OIPE

Does Not Comply
Corrected Diskette Needed

```
        RAW SEQUENCE LISTING                DATE: 10/22/2002
        PATENT APPLICATION:  US/09/966,264C    TIME: 09:29:03

        Input Set : N:\Crf4\10082002\I966264A.raw
        Output Set: N:\CRF4\10222002\I966264C.raw

   1 <110> APPLICANT: Barber, Elizabeth K
   2 <120> TITLE OF INVENTION: Gene Expression Control Element DNA
   3 <130> FILE REFERENCE: 896034605001
C-->  4 <140> CURRENT APPLICATION NUMBER: US/09/966,264C
   5 <141> CURRENT FILING DATE: 2001-09-28
   6 <150> PRIOR APPLICATION NUMBER: US 60/237,079
   7 <151> PRIOR FILING DATE: 2000-09-30
   8 <160> NUMBER OF SEQ ID NOS: 61
   9 <170> SOFTWARE: PatentIn version 3.1
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ERRORED SEQUENCES

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   566 <210> SEQ ID NO: 51
   567 <211> LENGTH: 1236
   568 <212> TYPE: DNA
   569 <213> ORGANISM: human
   570 <400> SEQUENCE: 51
E--> 571      tag ttt cct att caa tgt ata gtg cac caa agg tca att caa gag  -192
     572          Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu
     573              -75                 -70                 -65
E--> 574      ttt att att att att ttc aac cca agt aaa agc aga gag aaa ata gcc  -144
     575      Phe Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala
     576              -60                 -55                 -50
E--> 577      acc tcc acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg  -96
     578      Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu
     579              -45                 -40                 -35
E--> 580      aaa tga aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc  -48
     581      Lys     Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr
     582              -30                 -25                 -20
E--> 583      tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg gat ggt  0
     584      Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met Asp Gly
     585          -15                 -10                 -5
E--> 586      gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag  48
     587      Val Val     Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu
     588      1               5                   10                  15
E--> 589      taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc  96
     590          Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
     591                  20                  25                  30
E--> 592      atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga 144
     593      Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly
     594                  35                  40                  45
E--> 595      att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 192
```

cannot use negative numbers or φ
See § 1.822 (c)(6) of the new Rules,
37 CFR Part 1

RAW SEQUENCE LISTING   DATE: 10/22/2002
PATENT APPLICATION: US/09/966,264C   TIME: 09:29:03

Input Set : N:\Crf4\10082002\I966264A.raw
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```
        596     Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala     His
        597                     50                  55                  60
E--> 598     ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta 240
        599     Phe Ser Met     Thr Pro Val Ala     Ser Asn Ile Lys Leu Ile Leu
        600                     65                  70                  75
E--> 601     aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg 288
        602     Thr Asn Asn Val     Trp Leu His         Gly Phe Ala Ser Ser Trp
        603                     80                  85
E--> 604     aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt 336
        605     Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu
        606             90                  95                  100
E--> 607     ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa 384
        608     Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys
        609     105                 110                 115                 120
E--> 610     gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt 432
        611     Glu Thr Glu     Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe
        612                     125                 130                 135
E--> 613     ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg 480
        614     Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met
        615                     140                 145                 150
E--> 616     gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca 528
        617     Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr
        618                     155                 160                 165
E--> 619     gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat 576
        620     Asp Glu Glu Gly Ala Glu     Met Phe Tyr Asn Ser     Phe Pro His
        621                 170                 175                 180
E--> 622     ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt 624
        623     Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln     Glu Phe
        624                     185                 190                 195
E--> 625     aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt 672
        626     Thr Arg Asn Lys Ser Ile Phe Leu     Arg Val Val Val Leu Tyr Cys
        627                 200                 205                 210
E--> 628     aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag 720
        629     Arg Phe Gln     Phe Leu Ser Leu Leu Leu Phe Cys     Gln Trp Gln
        630                     215                 220                 225
E--> 631     gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca 768
        632     Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr
        633                     230                 235                 240
E--> 634     tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
        635     Cys Lys Ile Leu Ile Ala Lys     Leu Ala Ile Ser Leu Tyr Gly Thr
        636                     245                 250                 255
E--> 637     cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
        638     His Phe Gly Leu Phe Lys Asn Leu     Gln Leu     Arg Lys Asn Tyr
        639                     260                 265                 270
E--> 640     aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
        641     Lys Gly Lys Arg Lys     Arg Asn Gly Gln Val Val Lys Leu     Thr
        642                     275                 280
E--> 643     cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
        644     Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys     Gly Arg
```

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Input Set : **N:\Crf4\10082002\I966264A.raw**
Output Set: **N:\CRF4\10222002\I966264C.raw**

```
        645    285                 290                 295
E--> 646      aat agc atg aga agc cgt gtt tga tgt taa tta att            996
        647   Asn Ser Met Arg Ser Arg Val     Cys     Leu Ile
E--> 648      300                 305
        701 <210> SEQ ID NO: 55
        702 <211> LENGTH: 1236
        703 <212> TYPE: DNA
        704 <213> ORGANISM: human
        705 <400> SEQUENCE: 55
        706      ctagtttcct attcaatgta tagtgcacca aaggtcaatt caagagttta    50
        707      ttattattat tttcaaccca agtaaaagca gagagaaaat agccacctcc   100
        708      accatagcct cagaagcaag ccaacagcct gaaacagctt tgaaatgaaa   150
        709      agttggtgtg gcggtgatgg tggcagtgat aatggtgacc gatggttggg   200
E--> 710      tgctggtgat ggtagtggta gttgtgacag gtggtgatgg tggtttgatt   250
        711      gatagtaaaa aaaatgttcg ttaatacaag tagagagtaa gtaatcaatc   300
        712      aatcactcat agccaaggtg gaaaagatgt atcccatcat ggaatattcc   350
        713      tgttctgata gaaatcttgt gcttatctat ggaattcttt tgatatatat   400
        714      ttacattggg aacctgaatg tagcttgaca tttttccatg taaacaccag   450
        715      tagcctgatc caacattaag ctgatactaa caaacaacgt gtaatggctt   500
        716      cattaataag gctttgcttc ttcctggaaa ctggtgaaaa atcaaacctt   550
        717      gttgtgtaca ccctcgatgc agcttctgtg ttgtcttcac ccagaaatgg   600
        718      ggaatgattt cccaaatggc aaagaaacag agtgatgcta tctatctgca   650
        719      ccttttgtaa agtctgtctt tctttctctt tgttttccag gacacaatgt   700
        720      aggaagtctt ttccacatgg cagatgattt gggcagagcg atggagtcct   750
        721      tagtatcagt catgacagat gaagaaggag cagaataaat gttttacaac   800
        722      tcctgattcc cgcatggttt ttataatatt catacaacaa agaggattag   850
E--> 723      acagtaagag tttacaagaa atgaatcta tatttttgtg aagggtagtg   900
        724      gtattatact gtagatttca gtagtttcta agtctgttat tgttttgtta   950
        725      acaatggcag gttttacacg tctatgcaat tgtacaaaaa agttataaga  1000
        726      aaactacatg taaaatcttg atagctaaat aacttgccat ttctttatat  1050
        727      ggaacgcatt ttgggttgtt taaaaattta taacagttat aaagaaagaa  1100
        728      ttataaagga aaaagaaaat aacgcaatgg acaagtggtg aagctgtgaa  1150
        729      ctcaggtgtg cacaattatc aggaacaccc caaaaccaaa gtgaggtaga  1200
        730      aatagcatga gaagccgtgt ttgatgttaa ttaatt              1236
```

— must be represented by a nucleotide

VERIFICATION SUMMARY   DATE: 10/22/2002
PATENT APPLICATION: **US/09/966,264C**   TIME: 09:29:04

Input Set : **N:\Crf4\10082002\I966264A.raw**
Output Set: **N:\CRF4\10222002\I966264C.raw**

L:4 M:270 C: Current Application Number differs, Wrong Format
L:571 M:254 E: No. of Bases conflict, LENGTH:Input:-192 Counted:46 SEQ:51
M:254 Repeated in SeqNo=51
L:648 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1236 Found:1237 SEQ:51
L:710 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:723 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1